What is claimed is:

1. Process for the preparation of L-amino acids, in particular L-threonine, wherein the following steps are carried out:

   a) fermentation of the microorganisms of the Enterobacteriaceae family which produce the desired L-amino acid and in which the eno gene or nucleotide sequences or alleles which code for it are enhanced,

   b) concentration of the desired L-amino acid in the medium or in the cells of the microorganisms, and

   c) isolation of the desired L-amino acid, constituents of the fermentation broth and/or the biomass in its entirety or portions ($\geq$ 0 to 100%) thereof optionally remaining in the product.

2. Process according to claim 1, wherein microorganisms in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.

3. Process according to claim 1, wherein microorganisms in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.

4. Process according to claim 1, wherein the expression of the polynucleotide(s) which code(s) for the eno gene is increased.

5. Process according to claim 1, wherein the regulatory and/or catalytic properties of the polypeptide (protein) for which the polynucleotide eno codes are improved or increased.

6. Process for the preparation of L-amino acids according to claim 1, wherein microorganisms of the Enterobacteriaceae family in which additionally at the same time one or more of the genes chosen from the group consisting of:

6.1 the thrABC operon which codes for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase,

6.2 the pyc gene which codes for pyruvate carboxylase,

6.3 the pps gene which codes for phosphoenol pyruvate synthase,

6.4 the ppc gene which codes for phosphoenol pyruvate carboxylase,

6.5 the pntA and pntB genes which code for transhydrogenase,

6.6 the rhtB gene which imparts homoserine resistance,

6.7 the rhtC gene which imparts threonine resistance,

6.8 the thrE gene which codes for the threonine export protein,

6.9 the gdhA gene which codes for glutamate dehydrogenase,

6.10 the pgm gene which codes for phosphoglucomutase,

6.11 the fba gene which codes for fructose biphosphate aldolase,

6.12 the ptsH gene which codes for the phosphohistidine protein hexose phosphotransferase,

6.13 the ptsI gene which codes for enzyme I of the phosphotransferase system,

6.14 the crr gene which codes for the glucose-specific IIA component,

6.15 the ptsG gene which codes for the glucose-specific IIBC component,

6.16 the lrp gene which codes for the regulator of the leucine regulon,

6.17 the fadR which codes for the regulator of the fad regulon,

6.18 the iclR gene which codes for the regulator of central intermediate metabolism,

6.19 the ahpC gene which codes for the small sub-unit of alkyl hydroperoxide reductase,

6.20 the ahpF gene which codes for the large sub-unit of alkyl hydroperoxide reductase,

6.21 the cysK gene which codes for cysteine synthase A,

6.22 the cysB gene which codes for the regulator of the cys regulon,

6.23 the cysJ gene which codes for the flavoprotein of NADPH sulfite reductase,

6.24 the cysI gene which codes for the haemoprotein of NADPH sulfite reductase,

6.25 the cysH gene which codes for adenylyl sulfate reductase,

6.26 the rseA gene which codes for a membrane protein with anti-sigmaE activity,

6.27 the rseC gene which codes for a global regulator of the sigmaE factor,

6.28 the sucA gene which codes for the decarboxylase sub-unit of 2-ketoglutarate dehydrogenase,

6.29 the sucB gene which codes for the dihydrolipoyltranssuccinase E2 sub-unit of 2-ketoglutarate dehydrogenase,

6.30 the sucC gene which codes for the β-sub-unit of succinyl-CoA synthetase,

6.31 the sucD gene which codes for the α-sub-unit of succinyl-CoA synthetase,

6.32 the aceE gene which codes for the E1 component of the pyruvate dehydrogenase complex,

6.33 the aceF gene which codes for the E2 component of the pyruvate dehydrogenase complex, and

6.34 the rseB gene which codes for the regulator of sigmaE factor activity

is or are enhanced are fermented.

7. Process for the preparation of L-amino acids according to claim 1, wherein microorganisms of the Enterobacteriaceae family in which additionally at the same time one or more of the genes chosen from the group consisting of:

7.1 the tdh gene which codes for threonine dehydrogenase,

7.2 the mdh gene which codes for malate dehydrogenase,

7.3 the gene product of the open reading frame (orf) yjfA,

7.4 the gene product of the open reading frame (orf) ytfP,

7.5 the pckA gene which codes for phosphoenol pyruvate carboxykinase,

7.6 the poxB gene which codes for pyruvate oxidase,

7.7 the dgsA gene which codes for the DgsA regulator of the phosphotransferase system,

7.8 the fruR gene which codes for the fructose repressor,

7.9 the rpoS gene which codes for the sigma^{38} factor and

7.10 the aspA gene which codes for aspartate ammonium lyase

is or are attenuated, in particular eliminated or reduced in expression, are fermented.

8. Microorganisms of the Enterobacteriaceae family, in particular of the genus Escherichia, in which the eno gene or nucleotide sequences which code for it are present in enhanced form.

9. Microorganisms according to claim 8, wherein they produce L-threonine.